

[Exhibit A](#)**BLAST****Basic Local Alignment Search Tool**

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Blast 2 sequences

SEQ ID NO:1 vs. XM_044533Results for: ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID[|cl|46661](#)[|cl|46661](#)**Description**

None

Molecule type

amino acid

Query Length

837

Subject ID

46663

Description

None

Molecule type

amino acid

Subject Length

837

ProgramBLASTP 2.2.23+ [Citation](#)ReferenceStephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.Reference : compositional score matrix adjustmentStephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#)[Search Parameters](#)**Search parameter name Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hittlist size	100
Gapcosts	11,1

Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.320342	0.267
K	0.136493	0.041
H	0.42551	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

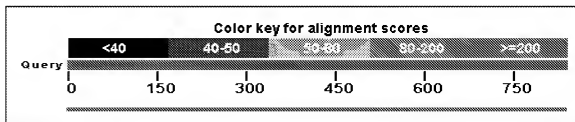
Effective search space	632025
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Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Dot Matrix View

Plot of lcl|46661 vs 46663 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
46663	unnamed protein product	1698	1698	100%	0.0	

Alignments

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)

>lcl|46663 unnamed protein product
Length=837

Score = 1698 bits (4398), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 831/837 (99%), Positives = 831/837 (99%), Gaps = 0/837 (0%)

Query	1	MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLQPPPTWALSPRISPLGSEERPFL	60
Sbjct	1	MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLQPPPTWALSPRISPLGSEERPFL	60
Query	61	RFEAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQCC	120
Sbjct	61	RFEAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQCC	120
Query	121	SFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLED	180
Sbjct	121	SFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLED	180
Query	181	GKGRCPDPNFKSTALVVDGELYTGTVSSFGQNDPAISRQSLRPTKTTESSLNWLQDPAF	240
Sbjct	181	GKGRCPDPNFKSTALVVDGELYTGTVSSFGQNDPAISRQSLRPTKTTESSLNWLQDPAF	240
Query	241	VASAYIPESLGSQGGDDKIYFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLLQQRW	300
Sbjct	241	VASAYIPESLGSQGGDDKIYFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLLQQRW	300
Query	301	TSFLKAQLLCSRDPDDGFFPNVLQDVFTLSPSPQDWRDTLFGYGVFTSQWHRGTTEGSACV	360
Sbjct	301	TSFLKAQLLCSRDPDDGFFPNVLQDVFTLSPSPQDWRDTLFGYGVFTSQWHRGTTEGSACV	360
Query	361	FTMKDVQRVFSGLYKEVNRETOQMVRHDPVPVTPRPGACITNSARERKINSSQLPDRVL	420
Sbjct	361	FTMKDVQRVFSGLYKEVNRETOQMVRHDPVPVTPRPGACITNSARERKINSSQLPDRVL	420

Query	421	NFLKDHFLMDGQVRSRMLLLQPQARYQRVAVHVRVPGHLHHTYDVFLGTGDGRLLHKAVSVG	480
		NFLKDHFLMDGQVRSRMLLLQPQARYQRVAVHVRVPGHLHHTYDVFLGTGDGRLLHKAVSVG	
Sbjct	421	NFLKDHFLMDGQVRSRMLLLQPQARYQRVAVHVRVPGHLHHTYDVFLGTGDGRLLHKAVSVG	480
Query	481	PRVHIIIEELQIFSSGQPVQNLDDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARD	540
		PRVHIIIEELQIFSSGQPVQNLDDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARD	
Sbjct	481	PRVHIIIEELQIFSSGQPVQNLDDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARD	540
Query	541	PYCAWSGSSCKHVSQYQPLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCQVQ	600
		PYCAWSGSSCKHVSQYQPLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCQVQ	
Sbjct	541	PYCAWSGSSCKHVSQYQPLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCQVQ	600
Query	601	FQPNVTNTLACPLLSNLATRLWLRNGAPVNASASCHVLPTGDLVVGTQQLGEFQCWSLE	660
		FQPNVTNTLACPLLSNLATRLWLRNGAPVNASASCHVLPTGDLVVGTQQLGEFQCWSLE	
Sbjct	601	FQPNVTNTLACPLLSNLATRLWLRNGAPVNASASCHVLPTGDLVVGTQQLGEFQCWSLE	660
Query	661	EGFQQLVASCYCEVVEDGVADQTDDEGGSVPVITISRVSAAPAGGKASWGADRSYWKFLV	720
		EGFQQLVASCYCEVVEDGVADQTDDEGGSVPVITISRVSAAPAGGKASWGADRSYWKFLV	
Sbjct	661	EGFQQLVASCYCEVVEDGVADQTDDEGGSVPVITISRVSAAPAGGKASWGADRSYWKFLV	720
Query	721	MCTLFVLAVLLPVFLLYRHRNSMKVFLKQGEACASVHPKTCPPVLPPEPRPLNGLGPPST	780
		MCTLFVLAVLLPVFLLYRHRNSMKVFLKQGEACASVHPKTCPPVLPPEPRPLNGLGPPST	
Sbjct	721	MCTLFVLAVLLPVFLLYRHRNSMKVFLKQGEACASVHPKTCPPVLPPEPRPLNGLGPPST	780
Query	781	PLDHRGYSLSDSPPGSRVFTSEKRPISQDSFVEVSPVCPRPVRVLGSEIRDSVV	837
		PLDHRGYSLSDSPPGSRVFTSEKRPISQDSFVEVSPVCPRPVRVLGSEIRDSVV	
Sbjct	781	PLDHRGYSLSDSPPGSRVFTSEKRPISQDSFVEVSPVCPRPVRVLGSEIRDSVV	837

Select All Get selected sequences Distance tree of results Multiple alignment